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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/844,705

DATE: 12/21/2001

TIME: 15:28:27

Input Set : N:\Crf3\RULE60\09844705.txt

Output Set: N:\CRF3\12212001\I844705.raw

5 <110> APPLICANT: BOSWORTH, BRAD
7 VOGELI, PETER
11 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
13 RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
17 <130> FILE REFERENCE: 21419/90368
19 <140> CURRENT APPLICATION NUMBER: 09/844,705
21 <141> CURRENT FILING DATE: 2001-04-27
23 <150> PRIOR APPLICATION NUMBER: 09/443,766
25 <151> PRIOR FILING DATE: 1999-11-19
29 <160> NUMBER OF SEQ ID NOS: 13
33 <170> SOFTWARE: PatentIn Ver. 2.0
37 <210> SEQ ID NO: 1
39 <211> LENGTH: 20
41 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
49 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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63 <211> LENGTH: 20
65 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
73 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
77 <400> SEQUENCE: 2
79 gtgcatggca ggctggatga 20
85 <210> SEQ ID NO: 3
87 <211> LENGTH: 22
89 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
97 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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109 <210> SEQ ID NO: 4
111 <211> LENGTH: 22
113 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
121 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
125 <400> SEQUENCE: 4
127 ttacctccag caggctatgg ac 22
133 <210> SEQ ID NO: 5
135 <211> LENGTH: 22
137 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence

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143 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
149 <400> SEQUENCE: 5
151 tccagagtgg agacaagtct.gc 22
157 <210> SEQ ID NO: 6
159 <211> LENGTH: 23
161 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
173 <400> SEQUENCE: 6
175 ctgcctgaac gtctatcaag atc 23
181 <210> SEQ ID NO: 7
183 <211> LENGTH: 22
185 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
197 <400> SEQUENCE: 7
199 agagttcct catgcccaca gg 22
205 <210> SEQ ID NO: 8
207 <211> LENGTH: 22
209 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
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223 ctgctacagg accaccagca tc 22
229 <210> SEQ ID NO: 9
231 <211> LENGTH: 35
233 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
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247 accagcagcg caaagtccct gacgggcacg gcctc 35
253 <210> SEQ ID NO: 10
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257 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
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277 <210> SEQ ID NO: 11
279 <211> LENGTH: 22
281 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:

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289 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
293 <400> SEQUENCE: 11
295 aactgcactg ccagttcat gc 22
301 <210> SEQ ID NO: 12
303 <211> LENGTH: 1269
305 <212> TYPE: DNA
307 <213> ORGANISM: Porcine
311 <220> FEATURE:
313 <221> NAME/KEY: CDS
315 <222> LOCATION: (9)..(1103)
319 <400> SEQUENCE: 12
321 ctcgagcc atg tgg gtc ccc agc cgc cgc cac ctc tgt ctg acc ttc ctg 50
323 Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu
325 1 5 10
329 cta gtc tgt gtt tta gca gca att ttc ttc ctg aac gtc tat caa gac 98
331 Leu Val Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp
333 15 20 25 30
337 ctc ttt tac agt ggc tta gac ctg ctg gcc ctg tgt cca gac cat aac 146
339 Leu Phe Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn
341 35 40 45
345 gtg gta tca tct ccc gtg gcc ata ttc tgc ctg gcg ggc acg ccg gta 194
347 Val Val Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val
349 50 55 60
353 cac ccc aac gcc tcc gat tcc tgt ccc aag cat cct gcc tcc ttt tcc 242
355 His Pro Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser
357 65 70 75
361 ggg acc tgg act att tac ccg gat ggc cgg ttt ggg aac cag atg gga 290
363 Gly Thr Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly
365 80 85 90
369 cag tat gcc acg ctg ctg gcc ctg gcg cag ctc aac ggc cgc cag gcc 338
371 Gln Tyr Ala Thr Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala
373 95 100 105 110
377 ttc atc cag cct gcc atg cac gcc gtc ctg gcc ccc gtg ttc cgc atc 386
379 Phe Ile Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile
381 115 120 125
385 acg ctg cct gtc ctg gcg ccc gag gta gac agg cac gct cct tgg cgg 434
387 Thr Leu Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg
389 130 135 140
393 gag ctg gag ctt cac gac tgg atg tcc gag gat tat gcc cac tta aag 482
395 Glu Leu Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys
397 145 150 155
401 gag ccc tgg ctg aag ctc acc ggc ttc ccc tgc tcc tgg acc ttc ttc 530
403 Glu Pro Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe
405 160 165 170
409 cac cac ctc cgg gag cag atc cgc agc gag ttc acc ctg cac gac cac 578
411 His His Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His
413 175 180 185 190
417 ctt cgg caa gag gcc cag ggg gta ctg agt cag ttc cgt cta ccc cgc 626
419 Leu Arg Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg

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421	195	200	205	
425	aca ggg gac cgc ccc agc acc ttc gtg ggg gtc cac gtg cgc cgc ggg			674
427	Thr Gly Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly			
429	210	215	220	
433	gac tat ctg cgt gtg atg ccc aag cgc tgg aag ggg gtg gtg ggt gac			722
435	Asp Tyr Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp			
437	225	230	235	
441	ggc cgt tac ctc cag cag gct atg gac tgg ttc cgg gcc cga tac gaa			770
443	Gly Arg Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu			
445	240	245	250	
449	gcc ccc gtc ttt gtg gtc acc agc aac ggc atg gag tgg tgc cgg aag			818
451	Ala Pro Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys			
453	255	260	265	270
457	aac atc gac acc tcc cgg ggg gac gtg atc ttt gct ggc gat ggg cgg			866
459	Asn Ile Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg			
461	275	280	285	
465	gag gcc gcg ccc gcc agg gac ttt gcg ctg ctg gtg cag tgc aac cac			914
467	Glu Ala Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His			
469	290	295	300	
473	acc atc atg acc att ggc acc ttc ggc ttc tgg gcc gcc tac ctg gct			962
475	Thr Ile Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala			
477	305	310	315	
481	ggt gga gat acc atc tac ttg gct aac ttc acc ctg ccc act tcc agc			1010
483	Gly Gly Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser			
485	320	325	330	
489	tcc ctg aag atc ttt aaa ccc gag gct gcc ttc ctg ccc gag tgg gtg			1058
491	Phe Leu Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val			
493	335	340	345	350
497	ggc att aat gca gac ttg tct cca ctc cag atg ttg gct ggg cct			1103
499	Gly Ile Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro			
501	355	360	365	
505	tgaaccagcc aggaggcttt ctggaatagc ctgcgtcaac ccagggccag cgttatgggt			1163
509	ctccggaaagc ccgagtaact tccggagatg ctgggtggcc tggacactta			1223
513	tttcaagagt gattctaatt ggctggactc agaggaaacc ctgcag			1269
519	<210> SEQ ID NO: 13			
521	<211> LENGTH: 365			
523	<212> TYPE: PRT			
525	<213> ORGANISM: Porcine			
529	<400> SEQUENCE: 13			
531	Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu Leu Val			
533	1	5	10	15
537	Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp Leu Phe			
539	20	25	30	
543	Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val			
545	35	40	45	
549	Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro			
551	50	55	60	
555	Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr			
557	65	70	75	80

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561 Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
563 85 90 95
567 Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile
569 100 105 110
573 Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu
575 115 120 125
579 Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu
581 130 135 140
585 Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro
587 145 150 155 160
591 Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
593 165 170 175
597 Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg
599 180 185 190
603 Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg Thr Gly
605 195 200 205
609 Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr
611 210 215 220
615 Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp Gly Arg
617 225 230 235 240
621 Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu Ala Pro
623 245 250 255
627 Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys Asn Ile
629 260 265 270
633 Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg Glu Ala
635 275 280 285
639 Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His Thr Ile
641 290 295 300
645 Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly
647 305 310 315 320
651 Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser Phe Leu
653 325 330 335
657 Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile
659 340 345 350
663 Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
665 355 360 365

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